

0590
1119

#5

OIPE

P.5

RAW SEQUENCE LISTING

DATE: 10/17/2001

PATENT APPLICATION: US/09/825,561A

TIME: 12:23:45

Input Set : A:\00-22SEQ.txt

Output Set: N:\CRF3\10172001\I825561A.raw

ENTERED

4 <110> APPLICANT: Sprecher, Cindy A.
 5 Novak, Julia E.
 6 West, James W.
 7 Presnell, Scott R.
 8 Holly, Richard D.
 9 Nelson, Andrew J.
 12 <120> TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
 15 <130> FILE REFERENCE: 00-22
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/825,561A
 C--> 17 <141> CURRENT FILING DATE: 2000-04-05
 17 <150> PRIOR APPLICATION NUMBER: US 60/194,731
 18 <151> PRIOR FILING DATE: 2000-04-05
 20 <150> PRIOR APPLICATION NUMBER: US 60/222,121
 21 <151> PRIOR FILING DATE: 2000-07-28
 23 <160> NUMBER OF SEQ ID NOS: 86
 25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1614
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)...(1614)
 36 <400> SEQUENCE: 1

37	atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg ctg ctg ctc cag gga	48
38	Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly	
39	1 5 10 15	
41	ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg	96
42	Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr	
43	20 25 30	
45	gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc	144
46	Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr	
47	35 40 45	
49	ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc	192
50	Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser	
51	50 55 60	
53	tgc agc ctc cac agg tgc gcc cac aat gcc acg cat gcc acc tac acc	240
54	Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr	
55	65 70 75 80	
57	tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc	288
58	Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val	
59	85 90 95	
61	aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt	336
62	Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe	
63	100 105 110	
65	ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg	384
66	Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val	

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67	115	120	125	
69	acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac	432		
70	Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp			
71	130	135	140	
73	cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac	480		
74	Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr			
75	145	150	155	160
77	agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc	528		
78	Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile			
79	165	170	175	
81	tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa	576		
82	Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys			
83	180	185	190	
87	gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc	624		
88	Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser			
89	195	200	205	
91	tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag	672		
92	Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln			
93	210	215	220	
95	acc cag tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt	720		
96	Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu			
97	225	230	235	240
99	ctc ctc ctg ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag	768		
100	Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys			
101	245	250	255	
103	acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc	816		
104	Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser			
105	260	265	270	
107	cct gag cgg ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc	864		
108	Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe			
109	275	280	285	
111	aag aaa tgg gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga	912		
112	Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly			
113	290	295	300	
115	ccc tgg agc cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac	960		
116	Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His			
117	305	310	315	320
119	cca cca cgg agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa	1008		
120	Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu			
121	325	330	335	
123	cca gca gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg	1056		
124	Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp			
125	340	345	350	
127	ccg aca gcc cag aac tcg ggg ggc tca gct tac agt gag gag agg gat	1104		
128	Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp			
129	355	360	365	
131	cgg cca tac ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca	1152		
132	Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala			
133	370	375	380	

RAW SEQUENCE LISTING

DATE: 10/17/2001

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TIME: 12:23:45

Input Set : A:\00-22SEQ.txt

Output Set: N:\CRF3\10172001\I825561A.raw

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135 gag ggg cca tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca      1200
136 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
137 385                      390                      395                      400
139 gcc ctg gac ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac      1248
140 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
141                      405                      410                      415
143 cca ctc ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca      1296
144 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
145                      420                      425                      430
147 gct ggc agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga      1344
148 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
149                      435                      440                      445
151 cta aag cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc      1392
152 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
153                      450                      455                      460
155 tgg ggt ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca      1440
156 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
157 465                      470                      475                      480
159 ccc ctg gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc      1488
160 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
161                      485                      490                      495
163 tct gac tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac      1536
164 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
165                      500                      505                      510
167 gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg      1584
168 Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
169                      515                      520                      525
173 cca ctt tcg agc cct gga ccc cag gcc agc      1614
174 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
175 530                      535
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 538
180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
183 <400> SEQUENCE: 2
184 Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Leu Gln Gly
185 1                      5                      10                      15
186 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
187                      20                      25                      30
188 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
189                      35                      40                      45
190 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
191                      50                      55                      60
192 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
193 65                      70                      75                      80
194 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
195                      85                      90                      95
196 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
197                      100                      105                      110

```

RAW SEQUENCE LISTING

DATE: 10/17/2001

PATENT APPLICATION: US/09/825,561A

TIME: 12:23:45

Input Set : A:\00-22SEQ.txt

Output Set: N:\CRF3\10172001\I825561A.raw

```

198 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
199      115      120      125
200 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
201      130      135      140
202 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
203 145      150      155      160
204 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
205      165      170      175
206 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
207      180      185      190
208 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
209      195      200      205
210 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
211      210      215      220
212 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
213 225      230      235      240
214 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
215      245      250      255
216 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
217      260      265      270
218 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
219      275      280      285
220 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
221      290      295      300
222 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
223 305      310      315      320
224 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
225      325      330      335
226 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
227      340      345      350
228 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
229      355      360      365
230 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
231      370      375      380
232 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
233 385      390      395      400
234 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
235      405      410      415
236 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
237      420      425      430
238 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
239      435      440      445
240 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
241      450      455      460
242 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
243 465      470      475      480
244 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
245      485      490      495
246 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp

```

RAW SEQUENCE LISTING

DATE: 10/17/2001

PATENT APPLICATION: US/09/825,561A

TIME: 12:23:45

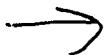
Input Set : A:\00-22SEQ.txt

Output Set: N:\CRF3\10172001\I825561A.raw

```

247          500          505          510
248  Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
249          515          520          525
250  Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
251          530          535
253 <210> SEQ ID NO: 3
254 <211> LENGTH: 696
255 <212> TYPE: DNA
256 <213> ORGANISM: Homo sapiens
259 <220> FEATURE:
260 <221> NAME/KEY: CDS
261 <222> LOCATION: (1)...(696)
263 <400> SEQUENCE: 3
264  ctg aac acg aca att ctg acg ccc aat ggg aat gaa gac acc aca gct      48
265  Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly Asn Glu Asp Thr Thr Ala
266   1          5          10          15
268  gat ttc ttc ctg acc act atg ccc act gac tcc ctc agt gtt tcc act      96
269  Asp Phe Phe Leu Thr Thr Met Pro Thr Asp Ser Leu Ser Val Ser Thr
270          20          25          30
272  ctg ccc ctc cca gag gtt cag tgt ttt gtg ttc aat gtc gag tac atg      144
273  Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met
274          35          40          45
276  aat tgc act tgg aac agc agc tct gag ccc cag cct acc aac ctc act      192
277  Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr
278   50          55          60
280  ctg cat tat tgg tac aag aac tcg gat aat gat aaa gtc cag aag tgc      240
281  Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys
282   65          70          75          80
284  agc cac tat cta ttc tct gaa gaa atc act tct ggc tgt cag ttg caa      288
285  Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln
286          85          90          95
288  aaa aag gag atc cac ctc tac caa aca ttt gtt gtt cag ctc cag gac      336
289  Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp
290          100          105          110
292  cca cgg gaa ccc agg aga cag gcc aca cag atg cta aaa ctg cag aat      384
293  Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn
294          115          120          125
296  ctg gtg atc ccc tgg gct cca gag aac cta aca ctt cac aaa ctg agt      432
297  Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser
298          130          135          140
302  gaa tcc cag cta gaa ctg aac tgg aac aac aga ttc ttg aac cac tgt      480
303  Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys
304          145          150          155          160
306  ttg gag cac ttg gtg cag tac cgg act gac tgg gac cac agc tgg act      528
307  Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr
308          165          170          175
310  gaa caa tca gtg gat tat aga cat aag ttc tcc ttg cct agt gtg gat      576
311  Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp
312          180          185          190

```


 Use of n and / or Xaa has been detected in the
 Sequence Listing. Review the Sequence Listing
 to ensure a corresponding explanation is present
 in the <220> to <223> fields of each sequence
 using n or Xaa.

VERIFICATION SUMMARY

DATE: 10/17/2001

PATENT APPLICATION: US/09/825,561A

TIME: 12:23:46

Input Set : A:\00-22SEQ.txt

Output Set: N:\CRF3\10172001\I825561A.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

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L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:2392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

L:2419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67

L:2578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71

L:2581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71